

**Table S14. *Clostridium innocuum* strain SB23 genes upregulated in the ceca of humanized mice fed the Western diet relative to the LF/PP diet.**

<b>Gene</b>	<b>Annotation</b>	<b>Fold-change<sup>a</sup></b>
SB23peg1618	hypothetical protein	28.4
SB23peg3176	hypothetical protein	27.4
SB23peg2539	hypothetical protein	25.6
SB23peg3431	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein oppA	16.8
SB23peg2353	hypothetical protein	16.5
SB23peg1766	hypothetical protein	16.0
SB23peg2795	hypothetical protein	14.5
SB23peg2556	hypothetical protein	14.0
SB23peg2540	hypothetical protein	14.0
SB23peg2541	hypothetical protein	12.3
SB23peg2547	hypothetical protein	11.8
SB23peg2555	hypothetical protein	11.5
SB23peg2542	hypothetical protein	11.0
SB23peg2444	1-deoxy-D-xylulose 5-phosphate synthase	10.9
SB23peg3365	acyl-coA dehydrogenase	10.6
SB23peg1482	Glycogen synthase, ADP-glucose transglucosylase	10.5
SB23peg315	hypothetical protein	10.4
SB23peg1003	Cytidylate kinase	10.0
SB23peg2932	Pyruvate formate-lyase	<b>9.5</b>
SB23peg209	transcriptional regulator, DeoR family	9.1
SB23peg1427	Phosphoglycerate kinase	<b>8.8</b>
SB23peg3636	coenzyme A transferase	8.6
SB23peg3366	hypothetical protein	8.4
SB23peg2651	PTS system N-acetylgalactosamine-specific IIC component	<b>8.0</b>
SB23peg2550	hypothetical protein	7.8
SB23peg3941	hypothetical protein	7.4
SB23peg3656	Ornithine carbamoyltransferase	7.0
SB23peg2935	Similar to ribosomal large subunit pseudouridine synthase D	6.5
SB23peg1557	hypothetical protein	6.1
SB23peg1526	hypothetical protein	6.0
SB23peg873	LSU ribosomal protein L3p	6.0
SB23peg2639	Hypothetical protein UPF0052	5.8
SB23peg2442	DNA repair protein RecN	5.3
SB23peg3102	PTS system, cellobiose-specific IIC component	<b>4.8</b>
SB23peg854	Preprotein translocase secY subunit	4.7
SB23peg3643	nitroreductase	4.7
SB23peg2938	Tagatose-6-phosphate kinase AgaZ	4.6
SB23peg2710	hypothetical protein	4.5
SB23peg840	hypothetical protein	4.4
SB23peg2245	Cell division trigger factor	4.1
SB23peg2827	LSU ribosomal protein L13p	4.1
SB23peg755	Protein-export membrane protein	3.9
SB23peg1907	SSU ribosomal protein S4p	3.7
SB23peg2702	ATPase, P-type (transporting), HAD superfamily, subfamily IC	3.6
SB23peg3986	ATP-dependent DNA helicase RecG	3.6
SB23peg2154	6-phosphofructokinase	<b>3.5</b>
SB23peg1051	2-enoate reductase	3.4
SB23peg851	Translation initiation factor 1	3.4
SB23peg4182	hypothetical protein	3.2
SB23peg2534	hypothetical protein	3.2

SB23peg2388	DNA primase	3.2
SB23peg382	hypothetical protein	3.1
SB23peg1577	Ribonucleotide reductase of class Ia (aerobic), beta subunit	3.1
SB23peg739	Transcription termination protein NusA	3.0
SB23peg1847	Catabolite control protein A	2.9
SB23peg2048	hypothetical protein	2.9
SB23peg1384	NADH-dependent butanol dehydrogenase A	2.9
SB23peg113	YjeF protein, function unknown	2.7
SB23peg2707	Multi antimicrobial extrusion protein (Na <sup>+</sup> )/drug antiporter	2.5
SB23peg774	transposase	2.5
SB23peg3443	Serine acetyltransferase	2.5
SB23peg1138	anaerobic nitric oxide reductase	<b>2.4</b>
SB23peg2041	Ribosomal large subunit pseudouridine synthase D	2.4
SB23peg2817	hypothetical protein	2.4
SB23peg3520	Dihydroorotate dehydrogenase electron transfer subunit	2.4
SB23peg780	hypothetical protein	2.3
SB23peg1355	alpha/beta hydrolase	<b>2.2</b>
SB23peg4122	Permease	2.2
SB23peg3059	Putative pheromone cAM373 precursor lipoprotein CamS	2.2

<sup>a</sup>Significant genes were identified using Cyber-T with the following criteria: p-value<0.001, PPDE(<p)>0.95, fold-change≥2, and ≥1 sequence observed in all samples from the up-regulated group.